AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

List of Claims:

Claims 1- 27 (cancelled)

Claim 28 (Currently amended): A method of simultaneously genotyping multiple samples in a single round of hybridization, the method comprising:

1) incubating a microarray of polynucleotide samples from multiple individuals with a single solution of a probe mixture of oligonucleotides of known sequence, wherein

a) the microarray contains a plurality of samples containing genotypes of interest with each sample in a distinct location ~~and~~, each location occupying an area smaller than or about 1 ~~square~~ millimeter across,

b) each sample has amplified polynucleotides with a defined segment containing a marker selected from a marker for a gene and markers for allelic variants of the gene,

c) the oligonucleotides in the probe mixture are of known sequence and length and have sequences specifically complementary to polynucleotide sequences within the defined segments for each sample for which a genotype is to be determined, wherein the oligonucleotides complementary to the polynucleotides are selected from the group consisting of oligonucleotides with sequences complementary to a segment containing the marker for (1) a gene, (2) one or more allelic variants of the gene, and (3) a gene and one or more allelic variants of the gene, and

d) the incubating forms hybrids of polynucleotides of the microarray and complementary oligonucleotides and allows discrimination at single nucleotide resolution; and

2) detecting at the distinct ~~location~~ locations on the microarray after a single round of hybridization, stable hybrids formed during the incubation, wherein a hybridization signal indicating the formation of a hybrid or lack of formation of a hybrid genotypes the ~~individual~~ individuals.

Claim 29 (previously presented): The method of claim 28 wherein the polynucleotide samples of the microarray are amplification products.

Claim 30 (previously presented): The method of claim 29, wherein the amplification products are produced by a polymerase chain reaction (PCR) method.

Claim 31 (previously amended): The method of claim 30 wherein the plurality of samples of polynucleotides is at least 10.

Claim 32 (previously presented): The method of claim 28 wherein an allele of the gene is associated with a disease.

Claim 33 (previously presented): The method of claim 32 wherein the disease is a human disease.

Claim 34 (previously presented): The method of claim 32 wherein the gene is human and is selected from the group consisting of β-globin, Cystic Fibrosis Transmembrane Conductance Regulator (CFTR), and Galactose-1-Phosphate Uridyltransferase (Gal-1-PU).

Claim 35 (previously presented): The method of claim 28 wherein the microarray is on a surface containing at least 1000 locations per square centimeter.

Claim 36 (previously amended): The method of claim 28 wherein the probe mixture of oligonucleotides of known sequence comprises oligonucleotides with ten different sequences.

Claim 37 (previously presented): The method of claim 28 wherein the oligonucleotides in the mixture are between about 10 and 30 nucleotides in length.

Claim 38 (previously presented): The method of claim 28 wherein the distinct segment is between about 40 and about 1000 nucleotides.

Claim 39 (previously presented): The method of claim 28 wherein the incubating is in an aqueous solution comprised of salts and detergent.

Claim 40 (previously presented): The method of claim 28 wherein hybridizing is performed at a temperature about 10 °C below the melting temperature of the stable hybrids.

Claim 41 (previously presented): The method of claim 28 wherein the oligonucleotides of known sequence are labeled.

Claim 42 (previously presented): The method of claim 41 wherein the label is fluorescent.

Claim 43 (previously presented): The method of claim 28, wherein samples from homozygotes and samples from heterozygotes are distinguishable.

Claim 44 (previously amended): The method of claim 28 wherein the plurality of samples of polynucleotides is at least 5,000.

Claim 45 (previously presented): The method of claim 28 wherein the individual specimens are neonatal blood samples.

Claim 46 (previously amended): The method of claim 28 wherein the individual is a human.

Claim 47 (New): A method of simultaneously genotyping multiple samples in a single round of hybridization, the method comprising:

1) incubating a microarray of polynucleotide samples from multiple individuals with a single solution of a probe mixture of oligonucleotides of known sequence, wherein

a) the microarray contains a plurality of samples containing genotypes of interest with each sample in a distinct location, wherein the microarray contains at least 60 sample locations per cm^2,

b) each sample has amplified polynucleotides with a defined segment containing a marker selected from a marker for a gene and markers for allelic variants of the gene,

c) the oligonucleotides in the probe mixture are of known sequence and length and have sequences specifically complementary to polynucleotide sequences within the defined segments for each sample for which a genotype is to be determined, wherein the oligonucleotides complementary to the polynucleotides are selected from the group consisting of oligonucleotides with sequences complementary to a segment containing the marker for (1) a gene, (2) one or more allelic variants of the gene, and (3) a gene and one or more allelic variants of the gene, and

d) the incubating forms hybrids of polynucleotides of the microarray and complementary oligonucleotides and allows discrimination at single nucleotide resolution; and

2) detecting at the distinct locations on the microarray after a single round of hybridization, stable hybrids formed during the incubation, wherein a hybridization signal indicating the formation of a hybrid or lack of formation of a hybrid genotypes the individuals.

Claim 48 (New): A method of simultaneously genotyping multiple samples in a single round of hybridization, the method comprising:

1) incubating a microarray of polynucleotide samples from multiple individuals with a single solution of a probe mixture of oligonucleotides of known sequence, wherein

a) the microarray contains a plurality of samples containing genotypes of interest with each sample in a distinct location on an impermeable support,

b) each sample has amplified polynucleotides with a defined segment containing a marker selected from a marker for a gene and markers for allelic variants of the gene,

c) the oligonucleotides in the probe mixture are of known sequence and length and have sequences specifically complementary to polynucleotide sequences within the defined segments for each sample for which a genotype is to be determined, wherein the oligonucleotides complementary to the polynucleotides are selected from the group consisting of oligonucleotides with sequences complementary to a segment containing the marker for (1) a gene, (2) one or more allelic variants of the gene, and (3) a gene and one or more allelic variants of the gene, and

d) the incubating forms hybrids of polynucleotides of the microarray and complementary oligonucleotides and allows discrimination at single nucleotide resolution; and

2) detecting at the distinct locations on the microarray after a single round of hybridization, stable hybrids formed during the incubation, wherein a hybridization signal indicating the formation of a hybrid or lack of formation of a hybrid genotypes the individuals.

Claim 49 (New): The method of claim 48, wherein the impermeable support further comprises an impermeable surface.

Claim 50 (New): The method of claim 48, wherein the impermeable support further comprises a permeable surface.

Claim 51 (New): The method of claim 48, wherein the impermeable support is rigid.

Claim 52 (New): The method of claim 48, wherein the impermeable support further comprises a surface comprising a reactive group that allows specific attachment of the amplified polynucleotides to the support.

Claim 53 (New): The method of claim 48 wherein the polynucleotide samples of the microarray are amplification products.

Claim 54 (New): The method of claim 53, wherein the amplification products are produced by a polymerase chain reaction (PCR) method.

Claim 55 (New): The method of claim 54 wherein the plurality of samples of polynucleotides is at least 10.

Claim 56 (New): The method of claim 48 wherein an allele of the gene is associated with a disease.

Claim 57 (New): The method of claim 56 wherein the gene is human and is selected from the group consisting of β-globin, Cystic Fibrosis Transmembrane Conductance Regulator (CFTR), and Galactose-1-Phosphate Uridyltransferase (Gal-1-PU).

Claim 58 (New): The method of claim 48 wherein the microarray is on a surface containing at least 1000 sample locations per square centimeter.

Claim 59 (New): The method of claim 48 wherein the probe mixture of oligonucleotides of known sequence comprises oligonucleotides with ten different sequences.

Claim 60 (New): The method of claim 48 wherein the oligonucleotides in the mixture are between about 10 and 30 nucleotides in length.

Claim 61 (New): The method of claim 48 wherein the distinct segment is between about 40 and about 1000 nucleotides.

Claim 62 (New): The method of claim 48 wherein hybridizing is performed at a temperature about 10°C below the melting temperature of the stable hybrids.

Claim 63 (New): The method of claim 48 wherein the oligonucleotides of known sequence are labeled.

Claim 64 (New): The method of claim 63 wherein the label is fluorescent.

Claim 65 (New): The method of claim 48, wherein samples from homozygotes and samples from heterozygotes are distinguishable.

Claim 66 (New): The method of claim 48 wherein the plurality of samples of polynucleotides is at least 5,000.

Claim 67 (previously presented): The method of claim 48 wherein the individual specimens are neonatal blood samples.

Claim 68 (New): The method of claim 48 wherein the individual is a human.